

SEQUENCE LISTING

<110> DE WAARD, Michel
 DUPUIS, Alain
 GRUNWALD, Didier
 SANDOZ, Guillaume

<120> CHIMERIC PROTEIN FOR THE SCREENING OF AGONISTS AND ANTAGONISTS OF
 CELL SIGNALLING PATHWAYS THAT ARE DEPENDENT ON G-PROTEIN-COUPLED
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<150> PCT/FR03/003860
 <151> 2003-12-22

<150> FR 02/16576
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<170> PatentIn version 3.3

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tca	gcc	gac	tcc	tac	acc	agc	cgc	ccc	tct	ctg	gac	tca	gac	gtt	tcc	96
Ser	Ala	Asp	Ser	Tyr	Thr	Ser	Arg	Pro	Ser	Leu	Asp	Ser	Asp	Val	Ser	
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ctg	gag	gag	gac	cgg	gag	agt	gcc	cgg	cga	gaa	gtg	gag	agt	cag	gct	144
Leu	Glu	Glu	Asp	Arg	Glu	Ser	Ala	Arg	Arg	Glu	Val	Glu	Ser	Gln	Ala	
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cag	cag	cag	ctg	gaa	aga	gcc	aag	cac	aaa	cct	gtg	gca	ttt	gct	gtg	192
Gln	Gln	Gln	Leu	Glu	Arg	Ala	Lys	His	Lys	Pro	Val	Ala	Phe	Ala	Val	
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Arg	Thr	Asn	Val	Ser	Tyr	Cys	Gly	Val	Leu	Asp	Glu	Glu	Cys	Pro	Val	
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Gln	Gly	Ser	Gly	Val	Asn	Phe	Glu	Ala	Lys	Asp	Phe	Leu	His	Ile	Lys	
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gag	aag	tac	agc	aat	gac	tgg	tgg	atc	ggg	agg	cta	gtg	aaa	gaa	ggc	336
Glu	Lys	Tyr	Ser	Asn	Asp	Trp	Trp	Ile	Gly	Arg	Leu	Val	Lys	Glu	Gly	
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Gly	Asp	Ile	Ala	Phe	Ile	Pro	Ser	Pro	Gln	Arg	Leu	Glu	Ser	Ile	Arg	
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ctc	aaa	cag	gaa	cag	aag	gcc	agg	aga	tcc	ggg	aac	cct	tcc	agc	ctg	432
Leu	Lys	Gln	Glu	Gln	Lys	Ala	Arg	Arg	Ser	Gly	Asn	Pro	Ser	Ser	Leu	
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Ser	Asp	Ile	Gly	Asn	Arg	Arg	Ser	Pro	Pro	Pro	Ser	Leu	Ala	Lys	Gln	
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Lys	Gln	Lys	Gln	Ala	Glu	His	Val	Pro	Pro	Tyr	Asp	Val	Val	Pro	Ser	
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Met	Arg	Pro	Val	Val	Leu	Val	Gly	Pro	Ser	Leu	Lys	Gly	Tyr	Glu	Val	
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Thr	Asp	Met	Met	Gln	Lys	Ala	Leu	Phe	Asp	Phe	Leu	Lys	His	Arg	Phe	
		195					200					205				
gat	ggc	agg	atc	tcc	atc	acc	cgc	gtc	acg	gct	gac	ctc	tca	ctg	gcc	672
Asp	Gly	Arg	Ile	Ser	Ile	Thr	Arg	Val	Thr	Ala	Asp	Leu	Ser	Leu	Ala	
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aag	cgc	tct	gtg	ctc	aac	aat	cct	ggc	aag	agg	acc	atc	atc	gag	cgc	720
Lys	Arg	Ser	Val	Leu	Asn	Asn	Pro	Gly	Lys	Arg	Thr	Ile	Ile	Glu	Arg	
225					230					235					240	
tct	tct	gcc	cgc	tcc	agc	att	gct	gag	gtg	cag	agt	gag	att	gag	cgc	768
Ser	Ser	Ala	Arg	Ser	Ser	Ile	Ala	Glu	Val	Gln	Ser	Glu	Ile	Glu	Arg	
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ata	ttc	gag	ctg	gcc	aaa	tcc	ctg	cag	cta	gtg	gtg	ttg	gat	gct	gac	816
Ile	Phe	Glu	Leu	Ala	Lys	Ser	Leu	Gln	Leu	Val	Val	Leu	Asp	Ala	Asp	
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cgc tcc agg ggg aag tcc cag atg aag cac ctc act gta cag atg atg Arg Ser Arg Gly Lys Ser Gln Met Lys His Leu Thr Val Gln Met Met 305 310 315 320	960
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cta gag gtt tac tgg cgc gct acc cac cac cca gca ccg ggc ccc ggg Leu Glu Val Tyr Trp Arg Ala Thr His His Pro Ala Pro Gly Pro Gly 355 360 365	1104
atg ctg ggt ccg ccc agt gcc atc cct gga ctt cag aac cag cag ctg Met Leu Gly Pro Pro Ser Ala Ile Pro Gly Leu Gln Asn Gln Gln Leu 370 375 380	1152
ctg ggg gag cga ggt gag gag cat tca ccc ctg gag cgg gac agt ttg Leu Gly Glu Arg Gly Glu Glu His Ser Pro Leu Glu Arg Asp Ser Leu 385 390 395 400	1200
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tct tca cag cgc agc tcc cgc cat ctg gag gag gac tat gca gat gcc Ser Ser Gln Arg Ser Ser Arg His Leu Glu Glu Asp Tyr Ala Asp Ala 420 425 430	1296
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gag cat gac cac aat gac cgg aac tgg cag cgt aac cgg cct tgg cct Glu His Asp His Asn Asp Arg Asn Trp Gln Arg Asn Arg Pro Trp Pro 465 470 475 480	1440
aag gac agc tac gaa ttc gcc aaa gaa agg gag cgg gtg gag aac cgg Lys Asp Ser Tyr Glu Phe Ala Lys Glu Arg Glu Arg Val Glu Asn Arg 485 490 495	1488
cgc gca ttc ctg aag ctg cgg cgg cag cag cag att gaa cgc gag ctc	1536

Arg	Ala	Phe	Leu	Lys	Leu	Arg	Arg	Gln	Gln	Gln	Ile	Glu	Arg	Glu	Leu		
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aac	ggg	tac	atg	gag	tgg	atc	tca	aaa	gca	gaa	gag	gtg	atc	ctc	gca		1584
Asn	Gly	Tyr	Met	Glu	Trp	Ile	Ser	Lys	Ala	Glu	Glu	Val	Ile	Leu	Ala		
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gag	gac	gag	acc	gac	gtg	gag	cag	aga	cat	ccc	ttt	gat	gga	gct	ctg		1632
Glu	Asp	Glu	Thr	Asp	Val	Glu	Gln	Arg	His	Pro	Phe	Asp	Gly	Ala	Leu		
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cgg	aga	gcc	act	atc	aag	aag	agc	aag	acg	gac	ctg	ctc	cac	cca	gag		1680
Arg	Arg	Ala	Thr	Ile	Lys	Lys	Ser	Lys	Thr	Asp	Leu	Leu	His	Pro	Glu		
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gag	gcg	gag	gat	cag	ctg	gcc	gac	atc	gcc	tcc	gtg	ggg	tct	ccc	ttt		1728
Glu	Ala	Glu	Asp	Gln	Leu	Ala	Asp	Ile	Ala	Ser	Val	Gly	Ser	Pro	Phe		
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gcc	cga	gcc	agc	att	aaa	agt	gcc	aag	ctg	gag	aac	tcg	agt	ttt	ttc		1776
Ala	Arg	Ala	Ser	Ile	Lys	Ser	Ala	Lys	Leu	Glu	Asn	Ser	Ser	Phe	Phe		
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cac	aaa	aaa	gag	agg	aga	atg	cgt	ttc	tac	atc	cgt	cgc	atg	gtc	aaa		1824
His	Lys	Lys	Glu	Arg	Arg	Met	Arg	Phe	Tyr	Ile	Arg	Arg	Met	Val	Lys		
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act	cag	taa															1833
Thr	Gln																
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<220>
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<400> 14

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			20					25					30				
Leu	Glu	Glu	Asp	Arg	Glu	Ser	Ala	Arg	Arg	Glu	Val	Glu	Ser	Gln	Ala		
		35					40					45					
Gln	Gln	Gln	Leu	Glu	Arg	Ala	Lys	His	Lys	Pro	Val	Ala	Phe	Ala	Val		
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Arg Thr Asn Val Ser Tyr Cys Gly Val Leu Asp Glu Glu Cys Pro Val
65 70 75 80

Gln Gly Ser Gly Val Asn Phe Glu Ala Lys Asp Phe Leu His Ile Lys
85 90 95

Glu Lys Tyr Ser Asn Asp Trp Trp Ile Gly Arg Leu Val Lys Glu Gly
100 105 110

Gly Asp Ile Ala Phe Ile Pro Ser Pro Gln Arg Leu Glu Ser Ile Arg
115 120 125

Leu Lys Gln Glu Gln Lys Ala Arg Arg Ser Gly Asn Pro Ser Ser Leu
130 135 140

Ser Asp Ile Gly Asn Arg Arg Ser Pro Pro Pro Ser Leu Ala Lys Gln
145 150 155 160

Lys Gln Lys Gln Ala Glu His Val Pro Pro Tyr Asp Val Val Pro Ser
165 170 175

Met Arg Pro Val Val Leu Val Gly Pro Ser Leu Lys Gly Tyr Glu Val
180 185 190

Thr Asp Met Met Gln Lys Ala Leu Phe Asp Phe Leu Lys His Arg Phe
195 200 205

Asp Gly Arg Ile Ser Ile Thr Arg Val Thr Ala Asp Leu Ser Leu Ala
210 215 220

Lys Arg Ser Val Leu Asn Asn Pro Gly Lys Arg Thr Ile Ile Glu Arg
225 230 235 240

Ser Ser Ala Arg Ser Ser Ile Ala Glu Val Gln Ser Glu Ile Glu Arg
245 250 255

Ile Phe Glu Leu Ala Lys Ser Leu Gln Leu Val Val Leu Asp Ala Asp
260 265 270

Thr Ile Asn His Pro Ala Gln Leu Ala Lys Thr Ser Leu Ala Pro Ile
275 280 285

Ile Val Phe Val Lys Val Ser Ser Pro Lys Val Leu Gln Arg Leu Ile
290 295 300

Arg Ser Arg Gly Lys Ser Gln Met Lys His Leu Thr Val Gln Met Met
305 310 315 320

Ala Tyr Asp Lys Leu Val Gln Cys Pro Pro Glu Ser Phe Asp Val Ile
325 330 335

Leu Asp Glu Asn Gln Leu Asp Asp Ala Cys Glu His Leu Ala Glu Tyr
340 345 350

Leu Glu Val Tyr Trp Arg Ala Thr His His Pro Ala Pro Gly Pro Gly
355 360 365

Met Leu Gly Pro Pro Ser Ala Ile Pro Gly Leu Gln Asn Gln Gln Leu
370 375 380

Leu Gly Glu Arg Gly Glu Glu His Ser Pro Leu Glu Arg Asp Ser Leu
385 390 395 400

Met Pro Ser Asp Glu Ala Ser Glu Ser Ser Arg Gln Ala Trp Thr Gly
405 410 415

Ser Ser Gln Arg Ser Ser Arg His Leu Glu Glu Asp Tyr Ala Asp Ala
420 425 430

Tyr Gln Asp Leu Tyr Gln Pro His Arg Gln His Thr Ser Gly Leu Pro
435 440 445

Ser Ala Asn Gly His Asp Pro Gln Asp Arg Leu Leu Ala Gln Asp Ser
450 455 460

Glu His Asp His Asn Asp Arg Asn Trp Gln Arg Asn Arg Pro Trp Pro
465 470 475 480

Lys Asp Ser Tyr Glu Phe Ala Lys Glu Arg Glu Arg Val Glu Asn Arg
485 490 495

Arg Ala Phe Leu Lys Leu Arg Arg Gln Gln Gln Ile Glu Arg Glu Leu
500 505 510

Asn Gly Tyr Met Glu Trp Ile Ser Lys Ala Glu Glu Val Ile Leu Ala

515

520

525

Glu Asp Glu Thr Asp Val Glu Gln Arg His Pro Phe Asp Gly Ala Leu
530 535 540

Arg Arg Ala Thr Ile Lys Lys Ser Lys Thr Asp Leu Leu His Pro Glu
545 550 555 560

Glu Ala Glu Asp Gln Leu Ala Asp Ile Ala Ser Val Gly Ser Pro Phe
565 570 575

Ala Arg Ala Ser Ile Lys Ser Ala Lys Leu Glu Asn Ser Ser Phe Phe
580 585 590

His Lys Lys Glu Arg Arg Met Arg Phe Tyr Ile Arg Arg Met Val Lys
595 600 605

Thr Gln
610